

SEQUENCE LISTING

<110> Mitsubishi Chemical Corporation

<120> A protein which is involved in recovery of cytoplasm male fertility from sterility and a gene encoding the protein

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195 200 205
Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr Gly Thr
210 215 220
Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala Leu Asn
225 230 235 240
Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn Val Val

245	250	255
Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg His Ser		
260	265	270
Asp Ala Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile Phe Pro		
275	280	285
Asp Leu Phe Thr Tyr Asn Ser Met Ile Val Gly Phe Cys Ser Ser Gly		
290	295	300
Arg Trp Ser Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu Arg Lys		
305	310	315
Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala Phe Val		
325	330	335
Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu Met Leu		
340	345	350
Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met Ile Asp		
355	360	365
Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met Phe Tyr		
370	375	380
Leu Met Ala Thr Lys Gly Cys Ser Pro Asn Leu Ile Thr Phe Asn Thr		
385	390	395
Leu Ile Asp Gly Tyr Cys Gly Ala Lys Arg Ile Asp Asp Gly Met Glu		
405	410	415
Leu Leu His Glu Met Thr Glu Thr Gly Leu Val Ala Asp Thr Thr Thr		
420	425	430
Tyr Asn Thr Leu Ile His Gly Phe Tyr Leu Val Gly Asp Leu Asn Ala		
435	440	445
Ala Leu Asp Leu Leu Gln Glu Met Ile Ser Ser Gly Leu Cys Pro Asp		
450	455	460

Ile Val Thr Cys Asp Thr Leu Leu Asp Gly Leu Cys Asp Asn Gly Lys
 465 470 475 480
 Leu Lys Asp Ala Leu Glu Met Phe Lys Val Met Gln Lys Ser Lys Lys
 485 490 495
 Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp Val Gln
 500 505 510
 Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys Phe Leu
 515 520 525
 Glu Ala Glu Glu Leu Tyr Glu Glu Met Pro His Arg Gly Ile Val Pro
 530 535 540
 Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys Gln Ser
 545 550 555 560
 Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser Lys Ser
 565 570 575
 Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asn Gly Tyr Cys
 580 585 590
 Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu Met Gly
 595 600 605
 Arg Arg Gly Ile Val Ala Asn Ala Ile Thr Tyr Ile Thr Leu Ile Cys
 610 615 620
 Gly Phe Arg Lys Val Gly Asn Ile Asn Gly Ala Leu Asp Ile Phe Gln
 625 630 635 640
 Glu Met Ile Ser Ser Gly Val Tyr Pro Asp Thr Ile Thr Ile Arg Asn
 645 650 655
 Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Ala Val Ala
 660 665 670
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675	680	685
<210> 4		
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<220>		
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<210> 5		
<211> 25		
<212> DNA		
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<220>		
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<400> 5		
ccaaaaatcc gaaatccgaa tagac		25
<210> 6		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
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<400> 6		
ctcggctctg gtttttagtga		20
<210> 7		
<211> 20		

<212> DNA
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<400> 7
tccacaaacc ctagccaaca 20
<210> 8
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<212> DNA
<213> Artificial Sequence
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<400> 8
gcttatgctt ctctggttcg cctc 24
<210> 9
<211> 27
<212> DNA
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<400> 9
ctcagtttc gtcaccttac acaatgc 27
<210> 10
<211> 23
<212> DNA
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<223> Description of Artificial Sequence: Synthetic DNA
<400> 10
gattcccttc tcttgcattt cag 23
<210> 11
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<400> 11
atctcgctt ttacattctg tgg 23
<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence
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<400> 12
cgggatccgc tcacaattt 18
<210> 13
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<400> 13
gcggatccca atttcattct gcatcactct ccctgtcggt atcgacacctg caaggttttt 60

gaaacggccg aaacgggaag tgacaatacc gctttctc 100
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<212> DNA
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cgaaaaaggt aatcatgcat ttatatgctg aagaaaagcg 100
<210> 15
<211> 3306
<212> DNA
<213> Raphanus sativus
<400> 15
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taataggtta gattttgggtt aggtctttct aattagtatg gagattctcg attccttctc 180
attgcagtgt ggtatgtcca actcattgtt tatgtacata tccaatttag ttttgagtca 240
aatgttagt tacttaagag ttgaatgaaa tagggatga tattgatggc caaggttctc 300
ccaaagtaaa taactttgtt tatattttaa gttagcttat aacatcaata aaaatgtcat 360
taactgggttc aataaaaaatg tcattaaactg gttcctctaa tataattatt taacacacct 420
ggctgttgat aaatttttat gatgtttaa taattttaga agtggatagt ctgttaatgg 480
tctttgattt gtcgtttga ttttaaaag tggactaaac aagaaggctt agtaataaat 540
actgaaccgg aactctactg gttcaatag ctgggttat caattctct cggctctggg 600
tttagtgaat catgtggccc tgtgggtta aacaaggaac tcaatcaatc aactggtgac 660
aatctgaac cgaaaattgt ataattcaaa ctgaaccggc tcttgtaaaa caaatggAAC 720

ccgtttgtac ttatctctc gtttatttc tcagtcacga gttttttta gagatcgacg 780
aagaacaaaa tttaggcgaa acaaaaataa aatgttggct agggttgtg gattcaagtg 840
ttcttcttct cctgctgagt ctgcggctag attgttctgt acgagatcga ttcgtgatac 900
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gcaaagtggg tttcatgaaa tcaaaggaaa agaggatgcg attgatttgc tcaagtgcacat 1020
gcttcgatct cgtcctttac cttctgtggt tgatttctgt aaattgtatgg gtgtgggt 1080
gagaatggaa cggccggatc ttgtgatttc tctctatcag aagatggaaa ggaaacagat 1140
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taagaaggaa gatactgtgt ctgcactgaa tctgctgagg aagatggagg aggtgagcca 1560
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tcatagcgat gcacaaaatc tttcactga aatgcaagag aaaggaatct ttcccgattt 1680
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<210> 16

<211> 2064

<212> DNA

<213> Raphanus sativus

<400> 16

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Met Leu Ala Arg Val Cys Gly Phe Lys Cys Ser Ser Ser Pro Ala Glu

1

5

10

15

tct gcg gct aga ttg ttc tgt acg aga tcg att cgt gat act ctg gcc 96

Ser Ala Ala Arg Leu Phe Cys Thr Arg Ser Ile Arg Asp Thr Leu Ala

20	25	30	
aag gca agc gga gag agt tgc gaa gca ggt ttt gga gga gag agt ttg 144			
Lys Ala Ser Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu Ser Leu			
35	40	45	
aag ctg caa agt ggg ttt cat gaa atc aaa ggt tta gag gat gcg att 192			
Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp Ala Ile			
50	55	60	
gat ttg ttc agt gac atg ctt cga tct cgt cct tta cct tct gtg gtt 240			
Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser Val Val			
65	70	75	80
gat ttc tgt aaa ttg atg ggt gtg gtg gtg aga atg gaa cgc ccg gat 288			
Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Glu Arg Pro Asp			
85	90	95	
ctt gtg att tct ctc tat cag aag atg gaa agg aaa cag att cga tgt 336			
Leu Val Ile Ser Leu Tyr Gln Lys Met Glu Arg Lys Gln Ile Arg Cys			
100	105	110	
gat ata tac agc ttc aat att ctg ata aaa tgt ttc tgc agc tgc tct 384			
Asp Ile Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser Cys Ser			
115	120	125	
aag ctc ccc ttt gct ttg tct aca ttt ggt aag ctc acc aag ctt gga 432			
Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Leu Thr Lys Leu Gly			
130	135	140	
ctc cac cct gat gtt gtt acc ttc acc acc ctg ctc cac gga ttg tgc 480			
Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly Leu Cys			
145	150	155	160
gtg gaa gat agg gtt tct gaa gct ttg aat ttg ttt cat caa atg ttt 528			
Val Glu Asp Arg Val Ser Glu Ala Leu Asn Leu Phe His Gln Met Phe			

165	170	175
gaa acg aca tgt agg ccc aat gtc gta acc ttc acc act ttg atg aac 576		
Glu Thr Thr Cys Arg Pro Asn Val Val Thr Phe Thr Thr Leu Met Asn		
180	185	190
ggt ctt tgc cgc gag ggt aga att gtc gaa gcc gta gct ctg ctt gat 624		
Gly Leu Cys Arg Glu Gly Arg Ile Val Glu Ala Val Ala Leu Leu Asp		
195	200	205
cgg atg atg gaa gat ggt ctc cag cct acc cag att act tat gga aca 672		
Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr Gly Thr		
210	215	220
atc gta gat ggg atg tgt aag aag gga gat act gtg tct gca ctg aat 720		
Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala Leu Asn		
225	230	235
ctg ctg agg aag atg gag gag gtg agc cac atc ata ccc aat gtt gta 768		
Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn Val Val		
245	250	255
atc tat agt gca atc att gat agc ctt tgt aaa gac gga cgt cat agc 816		
Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg His Ser		
260	265	270
gat gca caa aat ctt ttc act gaa atg caa gag aaa gga atc ttt ccc 864		
Asp Ala Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile Phe Pro		
275	280	285
gat tta ttt acc tac aac agt atg ata gtt ggt ttt tgt agc tct ggt 912		
Asp Leu Phe Thr Tyr Asn Ser Met Ile Val Gly Phe Cys Ser Ser Gly		
290	295	300
aga tgg agc gac gcg gag cag ttg ttg caa gaa atg tta gaa agg aag 960		
Arg Trp Ser Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu Arg Lys		

305	310	315	320
atc agc cct gat gtt gta act tat aat gct ttg atc aat gca ttt gtc	1008		
Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala Phe Val			
325	330	335	
aag gaa ggc aag ttc ttt gag gct gaa gaa tta tac gat gag atg ctt	1056		
Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu Met Leu			
340	345	350	
cca agg ggt ata atc cct aat aca atc aca tat agt tca atg atc gat	1104		
Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met Ile Asp			
355	360	365	
gga ttt tgc aaa cag aat cgt ctt gat gct gct gag cac atg ttt tat	1152		
Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met Phe Tyr			
370	375	380	
ttg atg gct acc aag ggc tgc tct ccc aac cta atc act ttc aat act	1200		
Leu Met Ala Thr Lys Gly Cys Ser Pro Asn Leu Ile Thr Phe Asn Thr			
385	390	395	400
ctc ata gac gga tat tgt ggg gct aag agg ata gat gat gga atg gaa	1248		
Leu Ile Asp Gly Tyr Cys Gly Ala Lys Arg Ile Asp Asp Gly Met Glu			
405	410	415	
ctt ctc cat gag atg act gaa aca gga tta gtt gct gac aca act act	1296		
Leu Leu His Glu Met Thr Glu Thr Gly Leu Val Ala Asp Thr Thr Thr			
420	425	430	
tac aac act ctt att cac ggg ttc tat ctg gtg ggc gat ctt aat gct	1344		
Tyr Asn Thr Leu Ile His Gly Phe Tyr Leu Val Gly Asp Leu Asn Ala			
435	440	445	
gct cta gac ctt tta caa gag atg atc tct agt ggt ttg tgc cct gat	1392		
Ala Leu Asp Leu Leu Gln Glu Met Ile Ser Ser Gly Leu Cys Pro Asp			

450	455	460
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Ile Val Thr Cys Asp Thr Leu Leu Asp Gly Leu Cys Asp Asn Gly Lys		
465	470	475
480		
cta aaa gat gca ttg gaa atg ttt aag gtt atg cag aag agt aag aag 1488		
Leu Lys Asp Ala Leu Glu Met Phe Lys Val Met Gln Lys Ser Lys Lys		
485	490	495
gat ctt gat gct agt cac ccc ttc aat ggt gtg gaa cct gat gtt caa 1536		
Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp Val Gln		
500	505	510
act tac aat ata ttg atc agc ggc ttg atc aat gaa ggg aag ttt tta 1584		
Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys Phe Leu		
515	520	525
530		
gag gcc gag gaa tta tac gag gag atg ccc cac agg ggt ata gtc cca 1632		
Glu Ala Glu Glu Leu Tyr Glu Glu Met Pro His Arg Gly Ile Val Pro		
535	540	
gat act atc acc tat agc tca atg atc gat gga tta tgc aag cag agc 1680		
Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys Gln Ser		
545	550	555
560		
cgc cta gat gag gct aca caa atg ttt gat tcg atg ggt agc aag agc 1728		
Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser Lys Ser		
565	570	575
580		
ttc tct cca aac gta gtg acc ttt act aca ctc att aat ggc tac tgt 1776		
Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asn Gly Tyr Cys		
585	590	
aag gca gga agg gtt gat gat ggg ctg gag ctt ttc tgc gag atg ggt 1824		
Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu Met Gly		

595	600	605	
cga aga ggg ata gtt gct aac gca att act tac atc act ttg att tgt 1872			
Arg Arg Gly Ile Val Ala Asn Ala Ile Thr Tyr Ile Thr Leu Ile Cys			
610	615	620	
ggt ttt cgt aaa gtg ggt aat att aat ggg gct cta gac att ttc cag 1920			
Gly Phe Arg Lys Val Gly Asn Ile Asn Gly Ala Leu Asp Ile Phe Gln			
625	630	635	640
gag atg att tca agt ggt gtg tat cct gat acc att acc atc cgc aat 1968			
Glu Met Ile Ser Ser Gly Val Tyr Pro Asp Thr Ile Thr Ile Arg Asn			
645	650	655	
atg ctg act ggt tta tgg agt aaa gag gaa cta aaa agg gca gtg gca 2016			
Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Ala Val Ala			
660	665	670	
atg ctt gag aaa ctg cag atg agt atg gat cta tca ttt ggg gga tga 2064			
Met Leu Glu Lys Leu Gln Met Ser Met Asp Leu Ser Phe Gly Gly Xaa			
675	680	685	
<210> 17			
<211> 688			
<212> PRT			
<213> Raphanus sativus			
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Ser Ala Ala Arg Leu Phe Cys Thr Arg Ser Ile Arg Asp Thr Leu Ala			
20	25	30	
Lys Ala Ser Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu Ser Leu			
35	40	45	

Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp Ala Ile
50 55 60
Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser Val Val
65 70 75 80
Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Glu Arg Pro Asp
85 90 95
Leu Val Ile Ser Leu Tyr Gln Lys Met Glu Arg Lys Gln Ile Arg Cys
100 105 110
Asp Ile Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser Cys Ser
115 120 125
Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Leu Thr Lys Leu Gly
130 135 140
Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly Leu Cys
145 150 155 160
Val Glu Asp Arg Val Ser Glu Ala Leu Asn Leu Phe His Gln Met Phe
165 170 175
Glu Thr Thr Cys Arg Pro Asn Val Val Thr Phe Thr Thr Leu Met Asn
180 185 190
Gly Leu Cys Arg Glu Gly Arg Ile Val Glu Ala Val Ala Leu Leu Asp
195 200 205
Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr Gly Thr
210 215 220
Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala Leu Asn
225 230 235 240
Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn Val Val
245 250 255
Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg His Ser

260	265	270
Asp Ala Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile Phe Pro		
275	280	285
Asp Leu Phe Thr Tyr Asn Ser Met Ile Val Gly Phe Cys Ser Ser Gly		
290	295	300
Arg Trp Ser Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu Arg Lys		
305	310	315
Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala Phe Val		
325	330	335
Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu Met Leu		
340	345	350
Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met Ile Asp		
355	360	365
Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met Phe Tyr		
370	375	380
Leu Met Ala Thr Lys Gly Cys Ser Pro Asn Leu Ile Thr Phe Asn Thr		
385	390	395
Leu Ile Asp Gly Tyr Cys Gly Ala Lys Arg Ile Asp Asp Gly Met Glu		
405	410	415
Leu Leu His Glu Met Thr Glu Thr Gly Leu Val Ala Asp Thr Thr Thr		
420	425	430
Tyr Asn Thr Leu Ile His Gly Phe Tyr Leu Val Gly Asp Leu Asn Ala		
435	440	445
Ala Leu Asp Leu Leu Gln Glu Met Ile Ser Ser Gly Leu Cys Pro Asp		
450	455	460
Ile Val Thr Cys Asp Thr Leu Leu Asp Gly Leu Cys Asp Asn Gly Lys		
465	470	475
		480

Leu Lys Asp Ala Leu Glu Met Phe Lys Val Met Gln Lys Ser Lys Lys
485 490 495
Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp Val Gln
500 505 510
Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys Phe Leu
515 520 525
Glu Ala Glu Glu Leu Tyr Glu Glu Met Pro His Arg Gly Ile Val Pro
530 535 540
Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys Gln Ser
545 550 555 560
Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser Lys Ser
565 570 575
Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asn Gly Tyr Cys
580 585 590
Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu Met Gly
595 600 605
Arg Arg Gly Ile Val Ala Asn Ala Ile Thr Tyr Ile Thr Leu Ile Cys
610 615 620
Gly Phe Arg Lys Val Gly Asn Ile Asn Gly Ala Leu Asp Ile Phe Gln
625 630 635 640
Glu Met Ile Ser Ser Gly Val Tyr Pro Asp Thr Ile Thr Ile Arg Asn
645 650 655
Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Ala Val Ala
660 665 670
Met Leu Glu Lys Leu Gln Met Ser Met Asp Leu Ser Phe Gly Gly Xaa
675 680 685

<211> 2073

<212> DNA

<213> Raphanus sativus

<400> 18

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tct gcg gct aga ttg ttc tgt acg aga tcg att cgt gat act ctg gcc 96
Ser Ala Ala Arg Leu Phe Cys Thr Arg Ser Ile Arg Asp Thr Leu Ala
20 25 30
aag gca agc agg gat gga gag agt tgc gaa gca ggt ttt gga gga gag 144
Lys Ala Ser Arg Asp Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu
35 40 45
agt ttg aag ctg caa agt ggg ttt cat gaa atc aaa ggt tta gag gat 192
Ser Leu Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp
50 55 60
gcg att gat ttg ttc agt gac atg ctt cga tct cgt cct tta cct tct 240
Ala Ile Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser
65 70 75 80
gtg gtt gat ttc tgt aaa ttg atg ggt gtg gtg gtg agg atg aaa cgc 288
Val Val Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Lys Arg
85 90 95
ccg gat gtt gtg att tct ctc cat aag aag atg gaa atg cgg cgc att 336
Pro Asp Val Val Ile Ser Leu His Lys Lys Met Glu Met Arg Arg Ile
100 105 110
cca tgt gat gca tac agc ttc aat att ctg ata aag tgt ttc tgc agc 384
Pro Cys Asp Ala Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser

115	120	125
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Cys Ser Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Leu Thr Lys		
130	135	140
ctt gga ctc cac cct gat gtt gtt acc ttc acc acc ctt ctc cac gga 480		
Leu Gly Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly		
145	150	155
ttg tgt gtg gaa aat agg ggt tct gaa gct ttg aat ttg ttt cat caa 528		
Leu Cys Val Glu Asn Arg Gly Ser Glu Ala Leu Asn Leu Phe His Gln		
165	170	175
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Met Phe Glu Thr Thr Cys Arg Pro Asn Val Val Thr Phe Thr Thr Leu		
180	185	190
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Met Asn Gly Leu Cys Arg Glu Gly Arg Ile Val Glu Ala Val Ala Leu		
195	200	205
ctt gat cgg atg atg gaa gat ggt ctc cag cct acc cag att act tat 672		
Leu Asp Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr		
210	215	220
gga aca atc gta gat ggg atg tgt aag aag gga gat act gtg tct gca 720		
Gly Thr Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala		
225	230	235
ctg aat ctg ctg agg aag atg gag gag gtg agc cac atc ata ccc aat 768		
Leu Asn Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn		
245	250	255
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Val Val Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg		

260	265	270
cat agc gat tct caa aat ctt ttc act gaa atg caa gag aaa gga atc 864		
His Ser Asp Ser Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile		
275	280	285
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Phe Pro Asp Leu Phe Thr Tyr Asn Cys Met Ile Asn Gly Phe Cys Ser		
290	295	300
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Ser Gly Arg Trp Ile Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu		
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Arg Lys Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala		
325	330	335
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370	375	380
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Phe Tyr Leu Met Pro Thr Lys Gly Cys Ser Pro Asp Val Phe Thr Phe		
385	390	395
aat act ctc ata gac gga tat cgt ggg gct aag agg ata gat gat gga 1248		
Asn Thr Leu Ile Asp Gly Tyr Arg Gly Ala Lys Arg Ile Asp Asp Gly		

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Val Thr Tyr Asn Thr Leu Ile His Gly Phe Cys Gln Val Gly Asp Leu		
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act gct gct cta gac ctt cta cat gag atg att tct agt ggt gtg tgc 1392		
Thr Ala Ala Leu Asp Leu Leu His Glu Met Ile Ser Ser Gly Val Cys		
450	455	460
cct aat gtc gtt act tgt agc act ttg ctg gat ggt ctc tgc gat aac 1440		
Pro Asn Val Val Thr Cys Ser Thr Leu Leu Asp Gly Leu Cys Asp Asn		
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Gly Lys Leu Lys Asp Ala Trp Glu Leu Phe Lys Val Met Gln Lys Ser		
485	490	495
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Lys Met Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp		
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gtt caa act tac aat ata ttg atc agc ggc ttg atc aat gaa ggg aag 1584		
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Gln Ser Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser			
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aag agc ttc tct cca aac gta gtg acc ttt act aca ctc att gat ggc 1776			
Lys Ser Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asp Gly			
580	585	590	
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Tyr Cys Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu			
595	600	605	
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610	615	620	
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Ile Arg Gly Phe Arg Asn Val Gly Asn Ile Asn Gly Ala Leu Asp Ile			
625	630	635	640
ttc cag gag atg att tca agt ggt gtg tat cct ggt atc att act atc 1968			
Phe Gln Glu Met Ile Ser Ser Gly Val Tyr Pro Gly Ile Ile Thr Ile			
645	650	655	
cgc agt atg ctg act ggt tta tgg agt aaa gag gaa cta aaa agg aca 2016			
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 35 40 45

Ser Leu Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp
 50 55 60

Ala Ile Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser
 65 70 75 80

Val Val Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Lys Arg
 85 90 95

Pro Asp Val Val Ile Ser Leu His Lys Lys Met Glu Met Arg Arg Ile
 100 105 110

Pro Cys Asp Ala Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser
 115 120 125

Cys Ser Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Leu Thr Lys
 130 135 140

Leu Gly Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly
 145 150 155 160

Leu Cys Val Glu Asn Arg Gly Ser Glu Ala Leu Asn Leu Phe His Gln

165	170	175
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Leu Asp Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr		
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245	250	255
Val Val Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg		
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His Ser Asp Ser Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile		
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Phe Pro Asp Leu Phe Thr Tyr Asn Cys Met Ile Asn Gly Phe Cys Ser		
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Ser Gly Arg Trp Ile Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu		
305	310	315
Arg Lys Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala		
325	330	335
Phe Val Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu		
340	345	350
Met Leu Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met		
355	360	365
Ile Asp Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met		
370	375	380

Phe Tyr Leu Met Pro Thr Lys Gly Cys Ser Pro Asp Val Phe Thr Phe
385 390 395 400
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405 410 415
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420 425 430
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435 440 445
Thr Ala Ala Leu Asp Leu Leu His Glu Met Ile Ser Ser Gly Val Cys
450 455 460
Pro Asn Val Val Thr Cys Ser Thr Leu Leu Asp Gly Leu Cys Asp Asn
465 470 475 480
Gly Lys Leu Lys Asp Ala Trp Glu Leu Phe Lys Val Met Gln Lys Ser
485 490 495
Lys Met Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp
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Leu His Gly Leu Cys Leu Asp Lys Arg Val Ser Glu Ala Leu Asp Leu
65 70 75 80
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Phe His Gln Met Phe Glu Thr Thr Cys Arg Pro Asn Ile Ile Thr Phe
85 90 95
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20

25

30

Phe Cys Ser Cys Ser Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys

35

40

45

Ile Thr Lys Leu Gly Leu His Pro Asp Val Ala Thr Phe Asn Thr Leu

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55

60

Leu His Gly Leu Cys Leu Asp Lys Arg Val Ser Glu Ala Leu Asp Leu

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75

80

Phe His Gln Met Phe Glu Thr Thr Cys Arg Pro Asn Ile Ile Thr Phe

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Thr Thr Leu Met Asn Gly Leu Cys Tyr Glu Gly Arg Val Val Glu Ala

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105

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Val Ala Leu Leu Asp Arg Met Leu Glu Asp Gly Leu Gln Pro Asp Gln

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Ala Ile Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser		
65	70	75
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Val Val Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Xaa Arg		
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Pro Asp Xaa Val Ile Ser Leu Xaa Xaa Lys Met Glu Xaa Xaa Xaa Ile		
100	105	110
Xaa Cys Asp Xaa Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser		
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Cys Ser Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Xaa Thr Lys		
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Leu Gly Leu His Pro Asp Val Xaa Thr Phe Xaa Thr Leu Leu His Gly		
145	150	155
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Leu Cys Xaa Xaa Xaa Arg Xaa Ser Glu Ala Leu Xaa Xaa Phe His Gln		
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Met Phe Glu Thr Thr Cys Arg Pro Asn Xaa Xaa Thr Phe Thr Thr Leu		
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Leu Asp Arg Met Xaa Glu Asp Gly Leu Gln Pro Xaa Gln Ile Thr Tyr		
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Gly Thr Ile Val Asp Gly Met Cys Lys Xaa Gly Asp Thr Val Ser Ala		
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Leu Asn Leu Leu Arg Lys Met Glu Glu Xaa Ser His Ile Xaa Pro Asn
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Val Val Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg
260 265 270
His Ser Asp Xaa Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile
275 280 285
Phe Pro Asp Leu Phe Thr Tyr Asn Xaa Met Ile Xaa Gly Phe Cys Ser
290 295 300
Ser Gly Arg Trp Xaa Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu
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Arg Lys Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala
325 330 335
Phe Val Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu
340 345 350
Met Leu Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met
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Ile Asp Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met
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Met Glu Leu Leu His Glu Met Thr Glu Xaa Gly Leu Val Ala Xaa Thr
420 425 430
Xaa Thr Tyr Asn Thr Leu Ile His Gly Phe Xaa Xaa Val Gly Asp Leu
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Pro Xaa Xaa Val Thr Cys Xaa Thr Leu Leu Asp Gly Leu Cys Asp Asn		
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Gly Lys Leu Lys Asp Ala Xaa Glu Xaa Phe Lys Val Met Gln Lys Ser		
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Lys Xaa Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp		
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Val Gln Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys		
515	520	525
Phe Leu Glu Ala Glu Glu Leu Tyr Xaa Glu Met Pro His Arg Gly Ile		
530	535	540
Val Pro Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys		
545	550	555
Gln Ser Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser		
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Lys Ser Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Xaa Gly		
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Tyr Cys Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu		
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Met Gly Arg Arg Gly Ile Val Ala Asn Xaa Ile Thr Tyr Ile Thr Leu		
610	615	620
Ile Xaa Gly Phe Arg Xaa Val Gly Asn Ile Asn Gly Ala Leu Asp Ile		
625	630	635
Phe Gln Glu Met Ile Ser Ser Gly Val Tyr Pro Xaa Xaa Ile Thr Ile		
645	650	655
Arg Xaa Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Xaa		
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35 40 45

Ser Leu Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp
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Ala Ile Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser
65 70 75 80
Val Val Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Xaa Arg
85 90 95
Pro Asp Xaa Val Ile Ser Leu Xaa Xaa Lys Met Glu Xaa Xaa Xaa Ile
100 105 110
Xaa Cys Asp Xaa Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser
115 120 125
Cys Ser Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Xaa Thr Lys
130 135 140
Leu Gly Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly
145 150 155 160
Leu Cys Val Glu Xaa Arg Xaa Ser Glu Ala Leu Xaa Xaa Phe His Gln
165 170 175
Met Phe Glu Thr Thr Cys Arg Pro Asn Val Val Thr Phe Thr Thr Leu
180 185 190
Met Asn Gly Leu Cys Arg Glu Gly Arg Ile Val Glu Ala Val Ala Leu
195 200 205
Leu Asp Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr
210 215 220
Gly Thr Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala
225 230 235 240
Leu Asn Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn
245 250 255
Val Val Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg

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Phe Pro Asp Leu Phe Thr Tyr Asn Xaa Met Ile Xaa Gly Phe Cys Ser		
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Ser Gly Arg Trp Xaa Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu		
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Arg Lys Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala		
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Phe Val Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu		
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Met Leu Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met		
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Ile Asp Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met		
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Gly Lys Leu Lys Asp Ala Xaa Glu Xaa Phe Lys Val Met Gln Lys Ser
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Lys Xaa Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp
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Val Pro Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys
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Gln Ser Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser
565 570 575
Lys Ser Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Xaa Gly
580 585 590
Tyr Cys Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu
595 600 605
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610 615 620
Ile Xaa Gly Phe Arg Xaa Val Gly Asn Ile Asn Gly Ala Leu Asp Ile
625 630 635 640
Phe Gln Glu Met Ile Ser Ser Gly Val Tyr Pro Xaa Xaa Ile Thr Ile
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25

30

Lys Ala Ser Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu Ser Leu

35

40

45

Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp Ala Ile

50

55

60

Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser Val Val

65

70

75

80

Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Glu Arg Pro Asp

85

90

95

Leu Val Ile Ser Leu Tyr Gln Lys Met Glu Arg Lys Gln Ile Xaa Cys

100

105

110

Asp Xaa Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser Cys Ser

115

120

125

Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Xaa Thr Lys Leu Gly

130	135	140
Leu His Pro Asp Val Xaa Thr Phe Xaa Thr Leu Leu His Gly Leu Cys		
145	150	155
Xaa Xaa Xaa Arg Val Ser Glu Ala Leu Xaa Xaa Phe His Gln Met Phe		
165	170	175
Glu Thr Thr Cys Arg Pro Asn Xaa Xaa Thr Phe Thr Thr Leu Met Asn		
180	185	190
Gly Leu Cys Xaa Glu Gly Arg Xaa Val Glu Ala Val Ala Leu Leu Asp		
195	200	205
Arg Met Xaa Glu Asp Gly Leu Gln Pro Xaa Gln Ile Thr Tyr Gly Thr		
210	215	220
Ile Val Asp Gly Met Cys Lys Xaa Gly Asp Thr Val Ser Ala Leu Asn		
225	230	235
Leu Leu Arg Lys Met Glu Glu Xaa Ser His Ile Xaa Pro Asn Val Val		
245	250	255
Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg His Ser		
260	265	270
Asp Ala Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile Phe Pro		
275	280	285
Asp Leu Phe Thr Tyr Asn Ser Met Ile Val Gly Phe Cys Ser Ser Gly		
290	295	300
Arg Trp Ser Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu Arg Lys		
305	310	315
Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala Phe Val		
325	330	335
Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu Met Leu		
340	345	350

Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met Ile Asp
355 360 365
Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met Phe Tyr
370 375 380
Leu Met Ala Thr Lys Gly Cys Ser Pro Asn Leu Ile Thr Phe Asn Thr
385 390 395 400
Leu Ile Asp Gly Tyr Cys Gly Ala Lys Arg Ile Asp Asp Gly Met Glu
405 410 415
Leu Leu His Glu Met Thr Glu Thr Gly Leu Val Ala Asp Thr Thr Thr
420 425 430
Tyr Asn Thr Leu Ile His Gly Phe Tyr Leu Val Gly Asp Leu Asn Ala
435 440 445
Ala Leu Asp Leu Leu Gln Glu Met Ile Ser Ser Gly Leu Cys Pro Asp
450 455 460
Ile Val Thr Cys Asp Thr Leu Leu Asp Gly Leu Cys Asp Asn Gly Lys
465 470 475 480
Leu Lys Asp Ala Leu Glu Met Phe Lys Val Met Gln Lys Ser Lys Lys
485 490 495
Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp Val Gln
500 505 510
Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys Phe Leu
515 520 525
Glu Ala Glu Glu Leu Tyr Glu Glu Met Pro His Arg Gly Ile Val Pro
530 535 540
Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys Gln Ser
545 550 555 560
Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser Lys Ser

	565	570	575
Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asn Gly Tyr Cys			
	580	585	590
Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu Met Gly			
	595	600	605
Arg Arg Gly Ile Val Ala Asn Ala Ile Thr Tyr Ile Thr Leu Ile Cys			
	610	615	620
Gly Phe Arg Lys Val Gly Asn Ile Asn Gly Ala Leu Asp Ile Phe Gln			
	625	630	635
Glu Met Ile Ser Ser Gly Val Tyr Pro Asp Thr Ile Thr Ile Arg Asn			
	645	650	655
Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Ala Val Ala			
	660	665	670
Met Leu Glu Lys Leu Gln Met Ser Met Asp Leu Ser Phe Gly Gly			
	675	680	685
<210> 29			
<211> 687			
<212> PRT			
<213> Raphanus			
<220>			
<221> Xaa			
<222> 140			
<223> Leu or Ile			
<221> Xaa			
<222> 170			
<223> Asn or Asp			
<221> Xaa			

<222> 171

<223> Leu or Phe

<400> 29

Met Leu Ala Arg Val Cys Gly Phe Lys Cys Ser Ser Ser Pro Ala Glu
1 5 10 15
Ser Ala Ala Arg Leu Phe Cys Thr Arg Ser Ile Arg Asp Thr Leu Ala
20 25 30
Lys Ala Ser Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu Ser Leu
35 40 45
Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp Ala Ile
50 55 60
Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser Val Val
65 70 75 80
Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Glu Arg Pro Asp
85 90 95
Leu Val Ile Ser Leu Tyr Gln Lys Met Glu Arg Lys Gln Ile Arg Cys
100 105 110
Asp Ile Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser Cys Ser
115 120 125
Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Xaa Thr Lys Leu Gly
130 135 140
Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly Leu Cys
145 150 155 160
Val Glu Asp Arg Val Ser Glu Ala Leu Xaa Xaa Phe His Gln Met Phe
165 170 175
Glu Thr Thr Cys Arg Pro Asn Val Val Thr Phe Thr Thr Leu Met Asn
180 185 190

Gly Leu Cys Arg Glu Gly Arg Ile Val Glu Ala Val Ala Leu Leu Asp
195 200 205
Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr Gly Thr
210 215 220
Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala Leu Asn
225 230 235 240
Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn Val Val
245 250 255
Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg His Ser
260 265 270
Asp Ala Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile Phe Pro
275 280 285
Asp Leu Phe Thr Tyr Asn Ser Met Ile Val Gly Phe Cys Ser Ser Gly
290 295 300
Arg Trp Ser Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu Arg Lys
305 310 315 320
Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala Phe Val
325 330 335
Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu Met Leu
340 345 350
Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met Ile Asp
355 360 365
Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met Phe Tyr
370 375 380
Leu Met Ala Thr Lys Gly Cys Ser Pro Asn Leu Ile Thr Phe Asn Thr
385 390 395 400
Leu Ile Asp Gly Tyr Cys Gly Ala Lys Arg Ile Asp Asp Gly Met Glu

405	410	415
Leu Leu His Glu Met Thr Glu Thr Gly Leu Val Ala Asp Thr Thr Thr		
420	425	430
Tyr Asn Thr Leu Ile His Gly Phe Tyr Leu Val Gly Asp Leu Asn Ala		
435	440	445
Ala Leu Asp Leu Leu Gln Glu Met Ile Ser Ser Gly Leu Cys Pro Asp		
450	455	460
Ile Val Thr Cys Asp Thr Leu Leu Asp Gly Leu Cys Asp Asn Gly Lys		
465	470	475
Leu Lys Asp Ala Leu Glu Met Phe Lys Val Met Gln Lys Ser Lys Lys		
485	490	495
Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp Val Gln		
500	505	510
Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys Phe Leu		
515	520	525
Glu Ala Glu Glu Leu Tyr Glu Glu Met Pro His Arg Gly Ile Val Pro		
530	535	540
Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys Gln Ser		
545	550	555
Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser Lys Ser		
565	570	575
Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asn Gly Tyr Cys		
580	585	590
Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu Met Gly		
595	600	605
Arg Arg Gly Ile Val Ala Asn Ala Ile Thr Tyr Ile Thr Leu Ile Cys		
610	615	620

Gly Phe Arg Lys Val Gly Asn Ile Asn Gly Ala Leu Asp Ile Phe Gln
625 630 635 640
Glu Met Ile Ser Ser Gly Val Tyr Pro Asp Thr Ile Thr Ile Arg Asn
645 650 655
Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Ala Val Ala
660 665 670
Met Leu Glu Lys Leu Gln Met Ser Met Asp Leu Ser Phe Gly Gly
675 680 685
<210> 30
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<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic DNA
<400> 30
acataaaaat cactagatac ttgacatgga ggc 33
<210> 31
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic DNA
<400> 31
aagaggagga agatggcatac acagc 25
<210> 32
<211> 26
<212> DNA

<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic DNA
<400> 32

tggagtaaag aggaactaaa aagggc 26
<210> 33
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic DNA
<400> 33

cagacaatag acgcataaaa ggc 23
<210> 34
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic DNA
<400> 34

gattccttc tcttgcattt cag 23
<210> 35
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 35
atctcgctt ttaccttctg tgg 23
<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic DNA
<400> 36
gatccatgca tttgtcaagg 20
<210> 37
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic DNA
<400> 37
catttgtgta gcctcatcta gg 22
<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic DNA
<400> 38
gtccggagag cagcccttgg tag 23
<210> 39

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 39

tcatcgata attcttcagc ctc 23

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 40

aaagacggac gtcataccga tg 22

<210> 41

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 41

gacatgttagg cccaatgtcg t 21